

RESULT 2

H98066 EKQERLAKLSGGAVYKGAETEKEMLRDEALNARAVEBIVGGPRLANV 420
 QY 421 IERVALELEGDTAGNTYVRALEPEVROTALNAGYEGSVVDRKLNSPAGTGENATG 480
 Db 421 IPAVATELTGTDEATRNTYVRALEEVROIAHAGFEGSTVDRKLNAELGIGPNATG 480

QY 481 EWDMKTKIILDKVTRSLQNAVASLILTEAVANKPEPATPAPAMPAGDPGM 540
 Db 481 EWDMKTKIILDKVTRSLQNAVASLILTEAVANKPEPATPAPAMPAGDPGM 540

QY 481 EWNNMDQGIDPVKVRSALQNAVASLILTEAVANKPEPATPAPAMPAGDPGM 540
 Db 481 EWNNMDQGIDPVKVRSALQNAVASLILTEAVANKPEPATPAPAMPAGDPGM 540

QY 541 GGM 543
 Db 537 GGM 539

RESULT 3

B86674 BD chaperonin [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 60 KD chaperonin [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Accession: B86674
 C;Species: Lactococcus lactis subsp. lactis
 C;Sequence_revision: 23-Mar-2001
 C;Date: 22-Oct-2001
 C;#sequence_change: 02-Nov-2001
 C;Accession: H98086
 R;Hobins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burnett, S.; Dehoff, B.S.; E
 e, R.; LeBanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McNamee, S.; M
 Y, P.; Sun, P.M.; Winkler, M.E.
 J.; Bacteriol. 183: 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A87872; MUID:2129245; PMID:1544234

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-40 <KU>
 A;Cross-references: GB:AE007317; PIDN:AM00525.1; PID:915459401; GSDB:GN00174
 A;Genetics:
 C;Superfamily: chaperonin groEL

Query Match 88.1%; Score 2347; DB 2; Length 540;
 Best Local Similarity 87.8%; Pred. No. 9.7e-110;
 Matches 477; Conservative 34; Mismatches 28; Indels 4; Gaps 1;

QY 1 MAKEIKFSADARAAWYGVMDLADTVKVLGPKGRNVLEKAFGSPPLITNDGYIAKEIE 60
 Db 1 MSKEIKFSSDARASAWKRGVDIDALTVKVLGPKGRNVLEKAFGSPPLITNDGYIAKEIE 60

QY 61 LEDHFENGMKJLSEVASKTKNDIAGSGTTATTLTDALYHEGKNTVAGANPIGIRGIE 120
 Db 61 LEDHFENGMKJLSEVASKTKNDIAGSGTTATTLTDALYHEGKNTVAGANPIGIRGIE 120

QY 121 TATATAVALKATRQPVSGEAKAQAVVASSRSEKVGYESAMERVGNDGVTIERSG 180
 Db 121 LARETAVASIKEAIPVHDSAIQAVVASSRSEKVGYESAMERVGSDGVTIERSG 180

QY 181 METELVEVGMDRGLSOMVTDNERKWDLENPFILDKVSNIODIPPLBEVK 240
 Db 181 MOPELVEVGMDRGLSOMVTDNERKWDLENPFILDKVSNIODIPPLBEVK 240

QY 241 TNRPLLIADDVGEALPTLVNKIRTFTVAVKAFGFCRKAMEDIAILALTGTVIT 300
 Db 301 EDGJLKDATTALGOAKITVYDSTVYEGSSSEAANRATLJKSOLETTSDFR 360

QY 361 EKQERLAKLSGGAVYKGAETEKEMLRDEALNARAVEBIVGGPRLANV 420
 Db 361 EKQERLAKLSGGAVYKGAETEKEMLRDEALNARAVEBIVGGPRLANV 420

QY 421 EDGJLKDATTALGOAKITVYDSTVYEGSSSEAANRATLJKSOLETTSDFR 360
 Db 421 IARDKLSBEGDQGTYNTVRALEEVROIAHAGFEGSTVDRKLNAELGIGPNATG 480

QY 481 EWDMKTKIILDKVTRSLQNAVASLILTEAVANKPEPATPAPAMPAGDPGM 540
 Db 481 EWDMKTKIILDKVTRSLQNAVASLILTEAVANKPEPATPAPAMPAGDPGM 540

QY 541 GGM 545
 Db 537 GMM 540

RESULT 4
JN0611
heat shock protein groEL - *Lactococcus lactis* subsp. *lactis*
C;Species: *Lactococcus lactis* subsp. *lactis*
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
R;Kim, S.G.; Bart, C.A.
Gene 127, 121-126, 1993
A;Title: Cloning and sequencing of *Lactococcus lactis* subsp. *lactis* groEL operon.
A;Reference number: JN0660; PMID:93252268; PMID:8486277
A;Molecule type: DNA
A;Residues: 1-542 <KIM>
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL
C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match Best Local Similarity 80.4%; Score 2171.5; DB 2; Length 542;
Matches 438; Conservative 53; Mismatches 49; Indels 5; Gaps 3;

Qy 1 MAKEKFSDARAKAMVRGVLMLADTVKTVGPCKRNVLEKAEGSPPLITNDVTAKEE 60
Db 1 MSKDIFKFSDDARTAMRGIDLADTVTGPCKRNVLEYSGSPLITNDVTAKEE 60
Qy 51 LEDHFMNGAKLVEASKTDINDGCTTATVLTQATVHGGKKVTAGANPIGRGIE 120
Db 61 LEVHFENNGAKLVEASKTDINDGCTTATVLTQATVHGGKKVTAGANPIGRGIE 120
Qy 121 TATAATVALKAIKAPVSGKEMIAQYAVASSSEKGVYISEAMERVGNDGVTIESRG 180
Db 121 LAETAVASIKEMAIPVHDKSIAQYAVATSSREKGVYISAMERVGSDGVITIESKG 180
Qy 181 METELEYVEKGKOPRGYLSQMYNTNEKVKADLRPLITDKVNSNQDITPYLEVK 240
Db 181 MOTEDVVEGKOPDRYLSQYMSNTEKVKADLRPLITDKKSNQDITPYLEVK 240
Qy 241 TRPDLITIADDVDPDRLATPLVNLKIRGTTTVAVKPGDRKAMLEDALITGGVIT 300
Db 241 TRPDLIVADYDVDPDRLATPLVNLKIRGTTTVAVKPGDRKAMLEDALITGGVIT 300
Qy 301 EDGLELKIDATMQLAQAKTVDSTWVGSSSEIANIAKIKQLETTSDFDR 360
Db 301 EEGLDLKDATLALGOAKATVDRHDTIVGASSADASDRAVIAKQIETTSDFDR 360
Qy 361 EKQERLAKLAGGAIVKVGAPTERALKEMKURIEDALNTRAIVEEGVWAGGTATV 420
Db 361 EKQERLAKLAGGAIVKVGAPTERALKEMKURIEDALNTRAIVEEGVWAGGTATV 420
Qy 421 TEKVAALVELEGDDATGKRVIALEPVRQILNNGEVSVIDKNSPAGGFNATG 480
Db 421 IALDKLSEGDIGIQTINIVRALLEPVRQILNNGEVSVIDKLSBEGVGFNATG 480
Qy 481 EWDMDIKGIDPKVTRSLONASVAVSLLTAAVANKPEPATPAPAMPMPGPM 540
Db 481 QWNMIEBGIIDPKVTRSLONASVAVSLLTAAVANKPEPATPAPAMPMPGPM 540
Qy 541 GGMG 545
Db 537 -GGG 540

RESULT 5
S32106
S32106
groEL protein - *Lactococcus lactis*
C;Species: *Lactococcus lactis*
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C;Accession: S32106
R;Bartt, C.A.
submitted to the EMBL Data Library, March 1993

A;Reference number: S32105
A;Accession: S32106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542
A;Cross-references: EMBL:X7132; NID:9287869; PID:CA5046.1; PID:9287871
C;Superfamily: chaperonin groEL

Query Match Best Local Similarity 80.4%; Score 2171.5; DB 2; Length 542;
Matches 438; Conservative 53; Mismatches 49; Indels 5; Gaps 3;

Qy 1 MAKEKFSDARAKAMVRGVLMLADTVKTVGPCKRNVLEKAEGSPPLITNDVTAKEE 60
Db 1 MSKDIFKFSDDARTAMRGIDLADTVTGPCKRNVLEYSGSPLITNDVTAKEE 60
Qy 61 LEDHFMNGAKLVEASKTDINDGCTTATVLTQATVHGGKKVTAGANPIGRGIE 120
Db 61 LEVHFENNGAKLVEASKTDINDGCTTATVLTQATVHGGKKVTAGANPIGRGIE 120
Qy 121 TATAATVALKAIKAPVSGKEMIAQYAVASSSEKGVYISEAMERVGNDGVTIESRG 180
Db 121 LAETAVASIKEMAIPVHDKSIAQYAVATSSREKGVYISAMERVGSDGVITIESKG 180
Qy 181 METELEYVEKGKOPRGYLSQMYNTNEKVKADLRPLITDKVNSNQDITPYLEVK 240
Db 181 MOTEDVVEGKOPDRYLSQYMSNTEKVKADLRPLITDKKSNQDITPYLEVK 240
Qy 241 TRPDLITIADDVDPDRLATPLVNLKIRGTTTVAVKPGDRKAMLEDALITGGVIT 300
Db 241 TRPDLIVADYDVDPDRLATPLVNLKIRGTTTVAVKPGDRKAMLEDALITGGVIT 300
Qy 301 EDGLELKIDATMQLAQAKTVDSTWVGSSSEIANIAKIKQLETTSDFDR 360
Db 301 EEGLDLKDATLALGOAKATVDRHDTIVGASSADASDRAVIAKQIETTSDFDR 360
Qy 361 EKQERLAKLAGGAIVKVGAPTERALKEMKURIEDALNTRAIVEEGVWAGGTATV 420
Db 361 EKQERLAKLAGGAIVKVGAPTERALKEMKURIEDALNTRAIVEEGVWAGGTATV 420
Qy 421 TEKVAALVELEGDDATGKRVIALEPVRQILNNGEVSVIDKNSPAGGFNATG 480
Db 421 IALDKLSEGDIGIQTINIVRALLEPVRQILNNGEVSVIDKLSBEGVGFNATG 480
Qy 481 EWDMDIKGIDPKVTRSLONASVAVSLLTAAVANKPEPATPAPAMPMPGPM 540
Db 481 QWNMIEBGIIDPKVTRSLONASVAVSLLTAAVANKPEPATPAPAMPMPGPM 540
Qy 541 GGMG 545
Db 537 -GGG 540

RESULT 6
A;0333
A;0333
C;Species: *Listeria monocytogenes*
C;Accession: ADJ333 #Sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
R;Slaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bj; D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fj; Science 294, 849-852, 2001
A;Authors: Kieft, J.; Kuhn, M.; Kunst, F.; Kuraphat, G.; Madueno, E.; Maitourna, O.; Schleiter, T.; Simoes, N.; Tarrer, A.; Vazquez-Boland, J.A.; Voss, H.; We
A;Title: Comparative genomics of *Listeria* species
A;Reference number: AB1077; PMID:2153729; PMID:11679669
A;Accession: ADJ333
A>Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542
A;Cross-references: GB-NC_003210; PID:CA00146.1; PID:916411538; GSDB:CN00177
A;Experimental source: strain EGD-e

Biosci. Biotechnol. Biochem. 56, 1995-2002, 1992
 A; Title: Isolation and characterization of the groES and groEL genes of *Bacillus subtilis*
 A; Reference number: JCI371; MUID:93129852; PMID:1369494
 A; Accession: JCI3712
 A; Molecule type: DNA
 A; Residues: 1-14, 'N', 16-124, 'L', 126-201, 'L', 203-374, 'R', 375-544 <P02>
 A; Cross-references: GB-D1097; GB-D01157; NID:943379; PIDN:BRASS2519.1; PID:94433781
 A; Experimental source: strain Marburg 168
 A; Note: the authors translated the codon ATT for residue 15 as Met
 R; Voeller, U.; Mach, H.; Schmidt, R.; Hecker, M.
 J. Gen. Microbiol. 138, 2125-2135, 1992
 A; Title: Stress proteins and cross-protection by heat shock and salt stress in *Bacillus*
 A; Reference number: A47683; MUID:93129863; PMID:1362210
 A; Contents: 1558
 A; Accession: B4683
 A; Molecule type: protein
 A; Residues: 2-31 <P02>
 A; Note: sequence extracted from NCBI backbone (NCBIP:121871)
 R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteletti, C.; Broni, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.; Chodat, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrall, E.; Nature 349, 256, 1997
 A; Authors: Fouarge, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Galli, L.; Ich, J.; Harwood, C.R.; Henaut, A.; Hibert, H.; Holzapfel, S.; Hosono, S.; Hulio, M.P.; Koetter, P.; Konstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Hardin, A.; Author: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portebeille, Rieger, M.; Rivolta, C.; Rocha, E.; Rose, M.; Sadde, Y.; Sato, T.; Scanlon, A.; Authors: Schleicher, S.; Schroeter, R.; Scrofano, P.; Sekiguchi, J.; Sekowska, A.; Seror, Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terashita, P.; Togomi, A.; Tosato, Y.; Uchiyama, T.; Winters, P.; Wapat, A.; Yamamoto, H.; Yamane, K.; Yamaoka, K.; Yoshida, K.; Authors: Yoshihara, H.F.; Zunstein, E.; Yoshihara, H.; Danchin, A.; Accession: D69637; A; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A; Reference number: A69580; MUID:9804033; PMID:938437
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-44 <SKUN>
 A; Cross-references: GB:Z99107; GB:AL009126; NID:92632866; PIDN:CAB12422.1; PID:92632916
 A; Experimental source: strain 168
 C; Genetics:
 A; Gene: groEL
 C; Superfamily: chaperonin groEL
 C; Keywords: heat shock, molecular chaperone; stress-induced protein
 Query Match 76.1%; Score 2026.5; DB 2; Length 544;
 Best Local Similarity 73.8%; Pred. No. 8.8e-94;
 Matches 402; Conservative 69; Mismatches 71; Indels 3; Gaps 1;
 Qy 1 MAKEKFSADARAAWVGRVYMLADTYKVTGPKGRNVLEKAFASPLITNDQVTAKEE 60
 Db 1 MAKEKFSADARAAWVGRVYMLADTYKVTGPKGRNVLEKAFASPLITNDQVTAKEE 60
 Qy 61 LEDFENNGAKLVSEVASKTDIADGTTATWLTAVTHEGKNTTACANPIGIRIGIE 120
 Db 61 LEDFENNGAKLVSEVASKTDIADGTTATWLTAVTHEGKNTTACANPIGIRIGIE 120
 Qy 121 TATAVAEALKIAQPSGKERAQYAAVSSRSKEVYISEMEERVGDVITIERS 180
 Db 121 TATAVAEALKIAQPSGKERAQYAAVSSRSKEVYISEMEERVGDVITIERS 180
 Qy 181 METELEVVEGNGQDFRGYLSQMVNTDNKVNADLENFILITDKVSNICDILPLLEVK 240
 Db 181 METELEVVEGNGQDFRGYLSQMVNTDNKVNADLENFILITDKVSNICDILPLLEVK 240
 Qy 241 TNRLPLIADQDGEALPTVLINKTRGPNVVAKAPGRGDRKAMLDIAITGGTV 300
 Db 241 TNRLPLIADQDGEALPTVLINKTRGPNVVAKAPGRGDRKAMLDIAITGGTV 300
 Qy 301 EDGELKLKDTMGLQAKYITKVDKSTVVEGSGSSEATANRALKSOLETTSDDR 360
 Db 301 EDGELKLKDTMGLQAKYITKVDKSTVVEGSGSSEATANRALKSOLETTSDDR 360
 Qy 361 EKLOERLAKLAGGVAVIKVGAPEETALKENKRLEDTNALNTRAVERGEGIVAGGGTALIV 420
 Db 361 EKLOERLAKLAGGVAVIKVGAPEETALKENKRLEDTNALNTRAVERGEGIVAGGGTALIV 420
 Qy 421 IEKVALALEGGDAQRNVLAPEPPVROIJALMAGEGSVIDLKNISPAGTCFNATG 480
 Db 421 IEKVALALEGGDAQRNVLAPEPPVROIJALMAGEGSVIDLKNISPAGTCFNATG 480
 Qy 481 ENWKVKGIGDPVWVTPSALONASASVSLITEAWANKPEPATAPAMPAGDMFMM 540
 Db 481 ENWKVKGIGDPVWVTPSALONASASVSLITEAWANKPEPATAPAMPAGDMFMM 537
 Qy 541 GGMGG 545
 Db 538 GGMGG 542

RESULT 9
 B49355
 heat shock protein GroEL - *Bacillus stearothermophilus*
 C; Species: *Bacillus stearothermophilus*
 C; Date: 07-Apr-1994 #text_change 18-Nov-1994 #text_change 12-Sep-1997
 C; Accession: B49835
 R; Schumann, U.; Schumann, W.; J. Bacteriol. 175, 2465-2469, 1993
 A; Title: Molecular cloning, sequencing, and transcriptional analysis of the groESL
 A; Reference number: A49835; MUID:9322474; PMID:8096841
 A; Status: preprint
 A; Molecule type: DNA
 A; Residues: 1-539 <SKUN>
 A; Note: sequence inconsistent with nucleotide translation
 A; Note: sequence extracted from NCBI backbone (NCBIP:129322, NCBIP:129324)
 C; Superfamily: chaperonin groEL
 Query Match 75.9%; Score 2021.5; DB 2; Length 539;
 Best Local Similarity 74.9%; Pred. No. 1.5e-93;
 Matches 408; Conservative 63; Mismatches 65; Indels 9; Gaps 2;
 Qy 1 MAKEKFSADARAAWVGRVYMLADTYKVTGPKGRNVLEKAFASPLITNDQVTAKEE 60
 Db 1 MAKEKFSADARAAWVGRVYMLADTYKVTGPKGRNVLEKAFASPLITNDQVTAKEE 60
 Qy 61 LEDFENNGAKLVSEVASKTDIADGTTATWLTAVTHEGKNTTACANPIGIRIGIE 120
 Db 61 LEDFENNGAKLVSEVASKTDIADGTTATWLTAVTHEGKNTTACANPIGIRIGIE 120
 Qy 121 TATAVAEALKIAQPSGKERAQYAAVSSRSKEVYISEMEERVGDVITIERS 180
 Db 121 TATAVAEALKIAQPSGKERAQYAAVSSRSKEVYISEMEERVGDVITIERS 180
 Qy 181 METELEVVEGNGQDFRGYLSQMVNTDNKVNADLENFILITDKVSNICDILPLLEVK 240
 Db 181 METELEVVEGNGQDFRGYLSQMVNTDNKVNADLENFILITDKVSNICDILPLLEVK 240
 Qy 241 TNRLPLIADQDGEALPTVLINKTRGPNVVAKAPGRGDRKAMLDIAITGGTV 300
 Db 241 TNRLPLIADQDGEALPTVLINKTRGPNVVAKAPGRGDRKAMLDIAITGGTV 300
 Qy 301 EDGELKLKDTMGLQAKYITKVDKSTVVEGSGSSEATANRALKSOLETTSDDR 360
 Db 301 EDGELKLKDTMGLQAKYITKVDKSTVVEGSGSSEATANRALKSOLETTSDDR 360
 Qy 361 EKLOERLAKLAGGVAVIKVGAPEETALKENKRLEDTNALNTRAVERGEGIVAGGGTALIV 420
 Db 361 EKLOERLAKLAGGVAVIKVGAPEETALKENKRLEDTNALNTRAVERGEGIVAGGGTALIV 420
 Qy 421 TERYAALERGDDATGNRIVNARALEEPYRQTLNAGYGSQVWIKLNNSPACTGFWANG 480
 Db 421 TERYAALERGDDATGNRIVNARALEEPYRQTLNAGYGSQVWIKLNNSPACTGFWANG 480
 Qy 481 EWDMKIGIDPVKVRSLAQNASASLITTRAVANKPEPATAPAMPAGMDGM- 539
 Db 481 EWDMKIGIDPVKVRSLAQNASASLITTRAVANKPEPATAPAMPAGMDGM- 539

RESULT 10

Db 481 EWDMDTEACIVDPDKVTRSLQHNSAASVAMLFTEAVADKPEE-----NKGGNCMP 533
 Qy 540 -NGGM 543
 |||
 Db 534 DNGM 538

JC6063 chaperonin groEL - *Bacillus* sp.
 ; species: *Bacillus* sp.
 C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 13-Sep-1998
 C; Accession: JG6063
 R; Xu, Y.; Zhou, P.J.
 Acta Microbiol. Sin. 36, 241-249, 1996
 A; Title: Phylogeny of molecular chaperone 60 proteins.
 A; Reference number: JG6063
 A; Molecule type: DNA
 A; Residues: 1-544 <XDR>
 A; Accession: JG6063
 A; Experimental source: strain C-125 strain BD224
 C; Genetics:
 A; Gene: groEL
 C; Superfamily: chaperonin groEL
 C; Keywords: molecular chaperone

Query Match 75.8%; Score 2017.5; DB 2; Length 544;
 Best Local Similarity 75.8%; Score 2017.5; DB 2; Length 544;
 Matches 400; Conservative 74; Mismatches 68; Indels 3; Gaps 1;

Qy 1 MAKIKESADSARAAVRGVDMLADTVKVTLGPKRNVLKARGSPPLITDGTYIKAKE 60
 Db 1 MAKDIKFSEDDARRSMRSGYDVKLADAVYTGPKGRNVLKFGSPPLITDGTYIKAKE 60

Qy 61 LEDFERNMGAKLVEASVAKTNDIAGDTTATVLOTAIHECKNTAGANPIGIRGIE 120
 Db 61 LEDFERNMGAKLVAEVASKTNDIAGDTTATVLOTAIHECKNTAGANPIGIRGIE 120

Qy 121 TATAFAVEALKAIQAVSKTDIAGDTTATVLOTAIHECKNTAGANPIGIRGIE 180
 Db 121 KATOVAVEELSKISKPIEGKSDIAQVAISADDVEGKILAEKERVNDGTYIESKG 180

Qy 181 METELEVYEGNQFDRLYQWYTDKVNADENPLITDKVSNQDPLIPLEEVLK 240
 Db 181 FSTELEVYEGNQFDRLYQWYTDKVNADENPLITDKVSNQDPLIPLEEVLK 240

Qy 241 TNRPLLIADDVGEALPTLVNLKTRGTFTNVAVKAPGFGDRKAMLDIAITGTWIT 300
 Db 241 OGKPLIILADDVGEALPTLVNLKTRGTFTNVAVKAPGFGDRKAMLDIAITGTWIT 300

Qy 301 EDGLGELKDATMQLCQAATKVDKOSTVIEVGSSSEATANRALKSQLETTSDFR 360
 Db 301 EDGLGDLKSANITQGRASKVWTKNTTVEGEGSDKIAARVNOKQIETTSDFK 360

Qy 361 EKLPLRIAKLAGVAVKQGAPTEALKMKURIEDLNTRRAVECGIVAGGGTALY 420
 Db 361 EKLPLRIAKLAGVAVKQGAPTEALKMKURIEDLNTRRAVECGIVAGGGTALY 420

Qy 421 IEKVALLELGSDATGRNVLVLAEPVQIANAGYEGSWVUDKLNSPAGTCFNAATG 480
 Db 421 IKAVSISIGEEDATGVNVNVLRAEPPVQSIANGAGLSYVERLKEEGFFNAATG 480

Qy 481 EWDMDTEACIVDPDKVTRSLQHNSAASVAMLFTEAVADKPEE-----NKGGNCMP 540
 Db 481 EWNVNYEAGIVDPDKVTRSLQHNSAASVAMLFTEAVADKPEE-----NKGGNCMP 537

RESULT 11

Db 541 GNGG 545
 ||||
 Db 538 GNGG 542

JG195 heat shock protein GroEL - thermophilic bacterium PS-3
 N; Alternative names: heat shock 61k protein; hsp60
 C; Species: thermophilic bacterium PS-3
 C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Sep-1997
 C; Accession: JG195; PC1252
 R; Tamaka, H.; Ohta, T.; Hamamoto, T.; Otawara-Hamamoto, Y.; Yanagi, M.; Hiraiwa, H.; Biochem. Biophys. Res. Commun. 179, 565-571, 1991
 A; Title: Gene structure of heat shock proteins 61kDa and 12kDa (Thermophilic Chaperon

A:Gene: groEL
C:Superfamily: chaperonin groEL

Query Match 71.5%; Score 1905; DB 2; Length 538;
Best Local Similarity 69.8%; Pred. No. 9.7e-88; Mismatches 83; Indels 2; Gaps 2;

Matches 377; Conservative 78; MisMatches 83; Index 2;

Oy 1 MAKEIKFSADARAAAMYGVDMALDTWVKTLPKGPNVLEKAFGSPLINDGTYTKEIE 60
Db 1 MYKOLKFSEDAAROAMLRGVDPOLANAVKVTIGPKGRNVPVNLKDFTAPLITNDGYTIKEIE 60
Oy 61 LEDPFENNGAKLVSEVASKNDIAGDGTTATVLTQATVHELIKNTAGANPIGGRGIE 120
Db 61 LEDPFENNGAKLVSEVASKNDIAGDGTTATVLTQATVHELIKNTAGANPIGGRGIE 120
Oy 121 TATATAVEALKAIQOPSGKERAQAVAVSSSEKVEYSEAMEERYGNOV--ITEE 17
Db 121 TATATAVEALKAIQOPSGKERAQAVAVSSSEKVEYSEAMEERYGNOV--ITEE 17
Oy 121 KAVKVAEALHENSOKNEKNEIAKVOGISAADEEGRYISATEKVNIDEVITIE 18
Db 121 KAVKVAEALHENSOKNEKNEIAKVOGISAADEEGRYISATEKVNIDEVITIE 18
Oy 181 METELEVUGMGGDGLSOMWMDNEKAUDENPFLITDKKNSFDIPLPQVO 240
Db 181 METELEVUGMGGDGLSOMWMDNEKAUDENPFLITDKKNSFDIPLPQVO 240
Oy 241 TURPLLIIDDVGAEALPTLVNKIRGTFPNVAKAPEGDRRKAMEDIALITGGTVR 300
Db 241 TURPLLIIDDVGAEALPTLVNKIRGTFPNVAKAPEGDRRKAMEDIALITGGTVR 300
Oy 241 METLQERLATAQSGAVVAKVKGAPPEATAKEMKLREDALNATRAAVEEGVARGGTLLTV 420
Db 241 METLQERLATAQSGAVVAKVKGAPPEATAKEMKLREDALNATRAAVEEGVARGGTLLTV 420
Oy 301 EDPLGLBLKDATMPALGQAQKITVDKDSPTVVEGGSSEBAINRLIKSQLETTDFDR 360
Db 301 DDLGLGLDKDASTIDMLGTTASKVETVTKDNTVVDGGDENSIDARVSOQLSQQETTESDFDR 360
Oy 361 ETLQERLATAQSGAVVAKVKGAPPEATAKEMKLREDALNATRAAVEEGVARGGTLLTV 420
Db 361 ETLQERLATAQSGAVVAKVKGAPPEATAKEMKLREDALNATRAAVEEGVARGGTLLTV 420
Oy 421 TEKVAELELEGDDATRTYRALLEEPRVQLAHVAGYGSVTDLKNSPACTGFNATG 480
Db 421 TEKVAELELEGDDATRTYRALLEEPRVQLAHVAGYGSVTDLKNSPACTGFNATG 480
Oy 481 ENWDKIQKIQIPKVTRSLQVQASASLTLTEAVVANIPPEPATPAPAMPGMPGM 540
Db 481 ENWDKIQKIQIPKVTRSLQVQASASLTLTEAVVANIPPEPATPAPAMPGMPGM 540
Oy 481 EWVNNLEAGIVDIPPTKVTSALQHRAVASVAMFLTEAVVASIPEKINDQPNM-GGM-PGM 538
Db 481 EWVNNLEAGIVDIPPTKVTSALQHRAVASVAMFLTEAVVASIPEKINDQPNM-GGM-PGM 538

RESULT 15
JN0001

heat shock protein 60 - staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
C:Accession: JN0001; PN0508
R:Orta, T.; Honda, K.; Kuroda, M.; Saito, K.; Hayashi, H.

BioChem. Biophys. Res. Commun. 193, 730-737, 1993
A:Title: Molecular characterization of the gene operon of heat shock proteins HSP60 and reference number: JN0001; Moid:93290669; PMID:7916607

A:Accession: JN0001
A:Accession: PN0508
A:Accession: PR0508
A:Molecule type: DNA
A:Residues: 1-539 <OH2>
A:Residues: 1-21 <OH2>
A:Genetics:
A:Genetics:
C:Genetics:
C:Genetics:
C:Keywords: heat shock; stress-induced protein

Query Match 69.4%; Score 1847.5; DB 2; Length 539;
Best Local Similarity 68.3%; Pred. No. 7.7e-85; Mismatches 7; Indels 7; Gaps 4;
Matches 371; Conservative 78; Mismatches 87; Index 7;

C:Keywords: heat shock; stress-induced protein